

## SEQUENCE LISTING

&lt;110&gt; FRAZER, IAN HECTOR

&lt;120&gt; A METHOD FOR OPTIMISING GENE EXPRESSION USING SYNONYMOUS CODON OPTIMISATION

&lt;130&gt; 21415-0015US

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<151> 2002-11-08

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&lt;210&gt; 1

&lt;211&gt; 714

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
humanized GFP sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(711)

&lt;400&gt; 1

agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg gaa  
Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu  
1 5 10 15

48

ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt  
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly  
20 25 30

96

gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc  
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr  
35 40 45

144

act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc tct  
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser  
50 55 60

192

tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat  
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His  
65 70 75 80

240

gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc	288		
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr			
85	90	95	
atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag	336		
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys			
100	105	110	
ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att gac	384		
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			
115	120	125	
ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat	432		
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr			
130	135	140	
aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc	480		
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile			
145	150	155	160
aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag	528		
Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln			
165	170	175	
ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg	576		
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val			
180	185	190	
ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa	624		
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys			
195	200	205	
gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc	672		
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr			
210	215	220	
gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga	714		
Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys			
225	230	235	
<210> 2			
<211> 237			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic humanized GFP sequence			
<400> 2			
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu			
1 5 10 15			
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly			
20 25 30			

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr  
 35 40 45

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser  
 50 55 60

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His  
 65 70 75 80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr  
 85 90 95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys  
 100 105 110

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp  
 115 120 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr  
 130 135 140

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile  
 145 150 155 160

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln  
 165 170 175

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val  
 180 185 190

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys  
 195 200 205

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr  
 210 215 220

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 3  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 3
      gca gca gca gca gca gca
      Ala Ala Ala Ala Ala Ala
      1           5

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 4
      Ala Ala Ala Ala Ala Ala
      1           5

<210> 5
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 5
      gcg gcg gcg gcg gcg gcg
      Ala Ala Ala Ala Ala Ala
      1           5

<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence
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<400> 6
Ala Ala Ala Ala Ala Ala
1 5

<210> 7
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 7
gct gct gct gct gct gct
Ala Ala Ala Ala Ala Ala
1 5 18

<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 8
Ala Ala Ala Ala Ala Ala
1 5

<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 9
gcc gcc gcc gcc gcc gcc
Ala Ala Ala Ala Ala Ala
1 5 18

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<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 10
Ala Ala Ala Ala Ala Ala
1                      5

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 11
aga aga aga aga aga aga
Arg Arg Arg Arg Arg Arg
1                      5          18

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 12
Arg Arg Arg Arg Arg Arg
1                      5

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

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<220>
<221> CDS
<222> (1)..(18)

<400> 13
cga cga cga cga cga cga
Arg Arg Arg Arg Arg Arg
1 5

18

<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 14
Arg Arg Arg Arg Arg Arg
1 5

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 15
cgg cgg cgg cgg cgg cgg
Arg Arg Arg Arg Arg Arg
1 5

18

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 16
Arg Arg Arg Arg Arg Arg
1 5

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<210> 17
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 17
cgt cgt cgt cgt cgt cgt
Arg Arg Arg Arg Arg Arg
1                      5

                                         18

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 18
Arg Arg Arg Arg Arg Arg
1                      5

<210> 19
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 19
agg agg agg agg agg agg
Arg Arg Arg Arg Arg Arg
1                      5

                                         18

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 20
Arg Arg Arg Arg Arg Arg
1          5

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 21
cgc cgc cgc cgc cgc cgc
Arg Arg Arg Arg Arg Arg
1          5

18

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 22
Arg Arg Arg Arg Arg Arg
1          5

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)
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<400> 23  
aac aac aac aac aac aac  
Asn Asn Asn Asn Asn Asn  
1 5 18

<210> 24  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<400> 24  
Asn Asn Asn Asn Asn Asn  
1 5

<210> 25  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<220>  
<221> CDS  
<222> (1)...(18)

<400> 25  
aat aat aat aat aat aat  
Asn Asn Asn Asn Asn Asn  
1 5 18

<210> 26  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<400> 26  
Asn Asn Asn Asn Asn Asn  
1 5

<210> 27  
<211> 18  
<212> DNA  
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 27
gat gat gat gat gat gat
Asp Asp Asp Asp Asp Asp
1 5

18

<210> 28
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 28
Asp Asp Asp Asp Asp Asp
1 5

<210> 29
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 29
gac gac gac gac gac gac
Asp Asp Asp Asp Asp Asp
1 5

18

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

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<400> 30
Asp Asp Asp Asp Asp Asp
1 5

<210> 31
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 31
tgc tgc tgc tgc tgc tgc 18
Cys Cys Cys Cys Cys Cys
1 5

<210> 32
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 32
Cys Cys Cys Cys Cys Cys
1 5

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 33
tgt tgt tgt tgt tgt tgt 18
Cys Cys Cys Cys Cys Cys
1 5

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<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 34
Cys Cys Cys Cys Cys Cys
1                      5

<210> 35
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 35
caa caa caa caa caa caa
Gln Gln Gln Gln Gln Gln
1                      5

18

<210> 36
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 36
Gln Gln Gln Gln Gln Gln
1                      5

<210> 37
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence
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<220>
<221> CDS
<222> (1)..(18)

<400> 37
cag cag cag cag cag cag
Gln Gln Gln Gln Gln Gln
1 5

18

<210> 38
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 38
Gln Gln Gln Gln Gln Gln
1 5

<210> 39
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 39
gaa gaa gaa gaa gaa
Glu Glu Glu Glu Glu Glu
1 5

18

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 40
Glu Glu Glu Glu Glu Glu
1 5

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<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 41
gag gag gag gag gag gag
Glu Glu Glu Glu Glu Glu
1 5

18

<210> 42
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 42
Glu Glu Glu Glu Glu Glu
1 5

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 43
gga gga gga gga gga gga
Gly Gly Gly Gly Gly Gly
1 5

18

<210> 44
<211> 6
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 44
Gly Gly Gly Gly Gly Gly
1          5

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 45
ggg ggg ggg ggg ggg ggg
Gly Gly Gly Gly Gly Gly
1          5

18

<210> 46
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 46
Gly Gly Gly Gly Gly Gly
1          5

<210> 47
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)
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<400> 47
ggc ggc ggc ggc ggc ggc
Gly Gly Gly Gly Gly Gly
1 5

18

<210> 48
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 48
Gly Gly Gly Gly Gly Gly
1 5

<210> 49
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 49
ggg ggg ggg ggg ggg ggg
Gly Gly Gly Gly Gly Gly
1 5

18

<210> 50
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 50
Gly Gly Gly Gly Gly Gly
1 5

<210> 51
<211> 18
<212> DNA
<213> Artificial Sequence

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<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<220>  
<221> CDS  
<222> (1)..(18)

<400> 51  
cac cac cac cac cac cac  
His His His His His His  
1 5

18

<210> 52  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<400> 52  
His His His His His His  
1 5

<210> 53  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<220>  
<221> CDS  
<222> (1)..(18)

<400> 53  
cat cat cat cat cat cat  
His His His His His His  
1 5

18

<210> 54  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

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<400> 54
His His His His His His
1 5

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 55
atc atc atc atc atc atc
Ile Ile Ile Ile Ile Ile
1 5 18

<210> 56
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 56
Ile Ile Ile Ile Ile Ile
1 5

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 57
att att att att att att
Ile Ile Ile Ile Ile Ile
1 5 18

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```

<210> 58
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 58
Ile Ile Ile Ile Ile Ile
1           5

<210> 59
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 59
ata ata ata ata ata ata
Ile Ile Ile Ile Ile Ile
1           5

18

<210> 60
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 60
Ile Ile Ile Ile Ile Ile
1           5

<210> 61
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

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```

<220>
<221> CDS
<222> (1)..(18)

<400> 61
ctc ctc ctc ctc ctc ctc
Leu Leu Leu Leu Leu Leu
1 5

18

<210> 62
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 62
Leu Leu Leu Leu Leu Leu
1 5

<210> 63
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 63
ttg ttg ttg ttg ttg ttg
Leu Leu Leu Leu Leu Leu
1 5

18

<210> 64
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 64
Leu Leu Leu Leu Leu Leu
1 5

```

```

<210> 65
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 65
cta cta cta cta cta cta
Leu Leu Leu Leu Leu Leu
1           5

18

<210> 66
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 66
Leu Leu Leu Leu Leu Leu
1           5

<210> 67
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 67
ctg ctg ctg ctg ctg ctg
Leu Leu Leu Leu Leu Leu
1           5

18

<210> 68
<211> 6
<212> PRT
<213> Artificial Sequence

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```
<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 68
Leu Leu Leu Leu Leu Leu
1           5

<210> 69
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 69
tta tta tta tta tta tta
Leu Leu Leu Leu Leu Leu
1           5

18

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 70
Leu Leu Leu Leu Leu Leu
1           5

<210> 71
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)
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<400> 71
ctt ctt ctt ctt ctt ctt
Leu Leu Leu Leu Leu Leu
1 5

18

<210> 72
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 72
Leu Leu Leu Leu Leu Leu
1 5

<210> 73
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 73
aag aag aag aag aag aag
Lys Lys Lys Lys Lys Lys
1 5

18

<210> 74
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 74
Lys Lys Lys Lys Lys Lys
1 5

<210> 75
<211> 18
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 75
aaa aaa aaa aaa aaa aaa
Lys Lys Lys Lys Lys Lys      18
1                               5

<210> 76
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 76
Lys Lys Lys Lys Lys Lys      18
1                               5

<210> 77
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 77
ttt ttt ttt ttt ttt ttt      18
Phe Phe Phe Phe Phe Phe      1     5

<210> 78
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

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<400> 78
Phe Phe Phe Phe Phe Phe
1 5

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 79
ttc ttc ttc ttc ttc ttc 18
Phe Phe Phe Phe Phe Phe
1 5

<210> 80
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 80
Phe Phe Phe Phe Phe Phe
1 5

<210> 81
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 81
ccc ccc ccc ccc ccc ccc 18
Pro Pro Pro Pro Pro Pro
1 5

```

<210> 82  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<400> 82  
Pro Pro Pro Pro Pro Pro  
1 5

<210> 83  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<220>  
<221> CDS  
<222> (1)...(18)

<400> 83  
cct cct cct cct cct  
Pro Pro Pro Pro Pro Pro  
1 5 18

<210> 84  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<400> 84  
Pro Pro Pro Pro Pro Pro  
1 5

<210> 85  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

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<220>
<221> CDS
<222> (1)..(18)

<400> 85
ccg ccg ccg ccg ccg ccg
Pro Pro Pro Pro Pro Pro
1 5

18

<210> 86
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 86
Pro Pro Pro Pro Pro Pro
1 5

<210> 87
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 87
cca cca cca cca cca cca
Pro Pro Pro Pro Pro Pro
1 5

18

<210> 88
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 88
Pro Pro Pro Pro Pro Pro
1 5

```

```

<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 89
      agc agc agc agc agc agc
      Ser Ser Ser Ser Ser Ser
      1                      5

                                         18

<210> 90
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 90
      Ser Ser Ser Ser Ser Ser
      1                      5

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 91
      tct tct tct tct tct tct
      Ser Ser Ser Ser Ser Ser
      1                      5

                                         18

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

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<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<400> 92  
Ser Ser Ser Ser Ser Ser  
1 5

<210> 93  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<220>  
<221> CDS  
<222> (1)..(18)

<400> 93  
agt agt agt agt agt agt  
Ser Ser Ser Ser Ser Ser  
1 5 18

<210> 94  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<400> 94  
Ser Ser Ser Ser Ser Ser  
1 5

<210> 95  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
leader sequence

<220>  
<221> CDS  
<222> (1)..(18)

<pre> &lt;400&gt; 95 tcg tcg tcg tcg tcg tcg Ser Ser Ser Ser Ser Ser 1 5 </pre> <pre> &lt;210&gt; 96 &lt;211&gt; 6 &lt;212&gt; PRT &lt;213&gt; Artificial Sequence </pre> <pre> &lt;220&gt; &lt;223&gt; Description of Artificial Sequence: Synthetic       leader sequence </pre> <pre> &lt;400&gt; 96 Ser Ser Ser Ser Ser Ser 1 5 </pre> <pre> &lt;210&gt; 97 &lt;211&gt; 18 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence </pre> <pre> &lt;220&gt; &lt;223&gt; Description of Artificial Sequence: Synthetic       leader sequence </pre> <pre> &lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (1)..(18) </pre> <pre> &lt;400&gt; 97 tca tca tca tca tca tca Ser Ser Ser Ser Ser Ser 1 5 </pre> <pre> &lt;210&gt; 98 &lt;211&gt; 6 &lt;212&gt; PRT &lt;213&gt; Artificial Sequence </pre> <pre> &lt;220&gt; &lt;223&gt; Description of Artificial Sequence: Synthetic       leader sequence </pre> <pre> &lt;400&gt; 98 Ser Ser Ser Ser Ser Ser 1 5 </pre> <pre> &lt;210&gt; 99 &lt;211&gt; 18 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence </pre>	18
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<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 99
tcc tcc tcc tcc tcc tcc
Ser Ser Ser Ser Ser
1 5

18

<210> 100
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 100
Ser Ser Ser Ser Ser
1 5

<210> 101
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 101
aca aca aca aca aca aca
Thr Thr Thr Thr Thr Thr
1 5

18

<210> 102
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

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<400> 102
Thr Thr Thr Thr Thr Thr
1 5

<210> 103
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 103
acg acg acg acg acg acg
Thr Thr Thr Thr Thr Thr
1 5 18

<210> 104
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 104
Thr Thr Thr Thr Thr Thr
1 5

<210> 105
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)...(18)

<400> 105
act act act act act act
Thr Thr Thr Thr Thr Thr
1 5 18

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```

<210> 106
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 106
Thr Thr Thr Thr Thr Thr
1                      5

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 107
acc acc acc acc acc acc
Thr Thr Thr Thr Thr Thr
1                      5

18

<210> 108
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 108
Thr Thr Thr Thr Thr Thr
1                      5

<210> 109
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

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<220>
<221> CDS
<222> (1)..(18)

<400> 109
tac tac tac tac tac tac
Tyr Tyr Tyr Tyr Tyr Tyr Tyr
1 5

18

<210> 110
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 110
Tyr Tyr Tyr Tyr Tyr Tyr
1 5

<210> 111
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 111
tat tat tat tat tat tat
Tyr Tyr Tyr Tyr Tyr Tyr Tyr
1 5

18

<210> 112
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 112
Tyr Tyr Tyr Tyr Tyr Tyr Tyr
1 5

```

```

<210> 113
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 113
gtg gtg gtg gtg gtg gtg
Val Val Val Val Val Val
1                      5

18

<210> 114
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 114
Val Val Val Val Val Val
1                      5

<210> 115
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 115
gtt gtt gtt gtt gtt gtt
Val Val Val Val Val Val
1                      5

18

<210> 116
<211> 6
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 116
      Val Val Val Val Val Val
      1           5

<210> 117
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

<400> 117
      gtc gtc gtc gtc gtc gtc
      Val Val Val Val Val Val
      1           5

18

<210> 118
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 118
      Val Val Val Val Val Val
      1           5

<210> 119
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<220>
<221> CDS
<222> (1)..(18)

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<400> 119
gta gta gta gta gta gta
Val Val Val Val Val Val
1 5

18

<210> 120
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      leader sequence

<400> 120
Val Val Val Val Val Val
1 5

<210> 121
<211> 2583
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(2166)

<400> 121
gaa ctt cgg gac gag caa act ccg ggc cac agg aag aac cca tcg aac 48
Glu Leu Arg Asp Glu Gln Thr Pro Gly His Arg Lys Asn Pro Ser Asn
1 5 10 15

caa agc agc tta gaa tct gac tcc aat tac ccc tcc att tcc act tcc 96
Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser
20 25 30

gaa atc gga gac act gag gat gcc ctt cag cag gtg gag gag att ggc 144
Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly
35 40 45

ata gag aag gca gcc atg gac atg acc gtc ttc ctg aag ctg cag aag 192
Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys
50 55 60

aga gtg cgc gaa ctt gag cag gag agg aag aag ctg cag gcg cag cta 240
Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys Leu Gln Ala Gln Leu
65 70 75 80

gaa aag gga cag cag gac agc aag aaa ggg cag gta gaa caa cag aac 288
Glu Lys Gly Gln Gln Asp Ser Lys Lys Gly Gln Val Glu Gln Gln Asn
85 90 95

aat ggc tta gat gtg gac cag gac gca gat ata gcc tac aat agt ctg 336
Asn Gly Leu Asp Val Asp Gln Asp Ala Asp Ile Ala Tyr Asn Ser Leu
100 105 110

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aag aga cag gag ctt gag tca gag aac aag aag ctg aag aat gac ctg	384
Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys Lys Leu Lys Asn Asp Leu	
115 120 125	
aat gag ctg agg aac ggt gtc gct gac caa gcc atg cag gat aac tcc	432
Asn Glu Leu Arg Asn Gly Val Ala Asp Gln Ala Met Gln Asp Asn Ser	
130 135 140	
acc cac agc tcc cca gac agc tac agc ctc cta ctg aac cag ctc aag	480
Thr His Ser Ser Pro Asp Ser Tyr Ser Leu Leu Asn Gln Leu Lys	
145 150 155 160	
ctg gcc aat gag gag ctc gag gtc cgc aaa gag gag gcg ctg atc ctc	528
Leu Ala Asn Glu Glu Leu Glu Val Arg Lys Glu Glu Ala Leu Ile Leu	
165 170 175	
agg acc cag atc atg aat gcc gac cag cgc cgc ctg tct ggc aag aac	576
Arg Thr Gln Ile Met Asn Ala Asp Gln Arg Arg Leu Ser Gly Lys Asn	
180 185 190	
atg gag ccg aac atc aat gcc aga aca agt tgg ccc aac agt gag aag	624
Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys	
195 200 205	
cac gtg gac cag gaa gac gcc att gag gcc tat cac ggg gtc tgc cag	672
His Val Asp Gln Glu Asp Ala Ile Glu Ala Tyr His Gly Val Cys Gln	
210 215 220	
aca aac agg ttg ctg gag gcc cag ctg cag gcc cag agc ctg gag cat	720
Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln Ala Gln Ser Leu Glu His	
225 230 235 240	
gag gag gag gtg gaa cat ctc aag gcc cag gtg gaa gcc ctg aaa gag	768
Glu Glu Glu Val Glu His Leu Lys Ala Gln Val Glu Ala Leu Lys Glu	
245 250 255	
gag atg gac aaa cag cag acc ttc tgc cag acc ctg ctg ctc tcc	816
Glu Met Asp Lys Gln Gln Gln Thr Phe Cys Gln Thr Leu Leu Leu Ser	
260 265 270	
cca gag gcc cag gta gaa ttt ggt gtc cag cag gag ata tcc cgg ctg	864
Pro Glu Ala Gln Val Glu Phe Gly Val Gln Gln Glu Ile Ser Arg Leu	
275 280 285	
acc aat gag aac ctg gat ttt aag gaa ttg gtg gaa aag ctg gag aag	912
Thr Asn Glu Asn Leu Asp Phe Lys Glu Leu Val Glu Lys Leu Glu Lys	
290 295 300	
aat gag agg aag ctg aag aag cag ctg aag att tac atg aag aag gtc	960
Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Val	
305 310 315 320	
cag gac tta gaa gct gcc cag gcg ttg gca cag agt gac agg agg cac	1008
Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala Gln Ser Asp Arg Arg His	
325 330 335	

cat gaa ctc aca aga cag gtc aca gtc caa cga aaa gag aag gac ttc	1056
His Glu Leu Thr Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe	
340 345 350	
caa ggc atg ctg gag tac cac aaa gag gtc gaa gcc ctc ctc atc cgg	1104
Gln Gly Met Leu Glu Tyr His Lys Glu Val Glu Ala Leu Leu Ile Arg	
355 360 365	
aac ctg gtg aca gac ctg aag cct cag atg ctg ctg ggc acc gtg ccc	1152
Asn Leu Val Thr Asp Leu Lys Pro Gln Met Leu Leu Gly Thr Val Pro	
370 375 380	
tgt ctg cct gca tac ata ctc tat atg tgc atc agg cac gac gat tac	1200
Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr	
385 390 395 400	
acc aac gat gac ctc aag gtg cac tcg ttg ctg agc tcc acc atc aac	1248
Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn	
405 410 415	
ggc att aag aaa gtc ctc aag aag cac aat gac gac ttt gag atg acg	1296
Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr	
420 425 430	
tca ttc tgg tta tcc aac acc tgc cgc ttc ctt cac tgt ctg aag caa	1344
Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln	
435 440 445	
tac agt ggt gat gag ggt ttc atg aca cag aac atc gcg aag cag aat	1392
Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn	
450 455 460	
gag cac tgt ctc aag aac ttt gac ctc act gaa tac cgc cag gta cta	1440
Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu	
465 470 475 480	
agc gac ctt tcc att cag atc tat cag cag ctc att aaa atg ccc gag	1488
Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu	
485 490 495	
ggc ttg cta cag cct atg ata gtt tct gcc atg ttg gaa aat gag agt	1536
Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser	
500 505 510	
atc cag ggg ctg tct ggt gtg aga cca act ggt tac cgg aag cgc tcc	1584
Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser	
515 520 525	
tcc agc atg gtg gat gga gag aat tct ttc cat aca gtc ctg tgt gac	1632
Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp	
530 535 540	
cag ggc ctg gac ccc gag att atc ctg cag gtg ttc aaa cag ctc ttc	1680
Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe	
545 550 555 560	

tac atg atc aat gct gtg act ctt aac aac cta ctc ctg cg <sup>g</sup> aaa gac Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys Asp 565 570 575	1728
gcc tgc tcc tgg agc aca ggc atg caa ctc agg tac aac ata agt caa Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln 580 585 590	1776
ctg gaa gag tgg ctt cg <sup>g</sup> ggc aaa aac ctt cac cag agt gga gca gtt Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val 595 600 605	1824
cag acc atg gag ccc ctg atc cag gca gcc cag ctc ctc cag ctg aag Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys 610 615 620	1872
aag aaa acc cac gag gat gct gag gcc atc tgc tct ctg tgc acc tcc Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser 625 630 635 640	1920
ctc agc acc cag cag att gtc aaa att tta aac ctc tac act ccc ttg Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu 645 650 655	1968
aat gaa ttt gag gaa cg <sup>g</sup> gtc aca gtg tcc ttc atc aga aca atc cag Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln 660 665 670	2016
gct cag cta caa gag agg aat gac cct cag cag ctc ctg ctg gac tcc Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser 675 680 685	2064
aag cac gtg ttc cca gtt ctg ttt cca tat aac cca tct gct ctg acc Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr 690 695 700	2112
atg gac tcg atc cac atc ccg gcc tgt ctc aac ctg gag ttt ctc aat Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn 705 710 715 720	2160
gaa gtc tgaggatgcg tgttccgag gcgagcgaga aggaagcatg tgctgtcagc Glu Val	2216
cgagagaatg ctaggtgtgt taaatattcc agcgtagatc aaaccatgtt agagactggc gggacgacag aactaaacag cgggggtgcac agttgtcgcc aatgctgctc agaaaacacc cggaagtgga ttgtttaaag ctgtgcttcc aggttaaacc aagacacg <sup>t</sup> c agaacgaaca gccactctgc agctccagtc gccatataaa aatgccagtt ctacagagt <sup>g</sup> gaagtgccta gctttgatct ttgtatatat cttgagaatg ttcaaactga gataatatta aaaacacatg acgtaaattg ctttgcggg tcttcaaga aatgatggg ctaataacca taagattgac aggaatt	2276 2336 2396 2456 2516 2576 2583

<210> 122  
 <211> 722  
 <212> PRT  
 <213> Mus sp.

<400> 122  
 Glu Leu Arg Asp Glu Gln Thr Pro Gly His Arg Lys Asn Pro Ser Asn  
 1 5 10 15

Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser  
 20 25 30

Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly  
 35 40 45

Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys  
 50 55 60

Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys Leu Gln Ala Gln Leu  
 65 70 75 80

Glu Lys Gly Gln Gln Asp Ser Lys Lys Gly Gln Val Glu Gln Gln Asn  
 85 90 95

Asn Gly Leu Asp Val Asp Gln Asp Ala Asp Ile Ala Tyr Asn Ser Leu  
 100 105 110

Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys Lys Leu Lys Asn Asp Leu  
 115 120 125

Asn Glu Leu Arg Asn Gly Val Ala Asp Gln Ala Met Gln Asp Asn Ser  
 130 135 140

Thr His Ser Ser Pro Asp Ser Tyr Ser Leu Leu Leu Asn Gln Leu Lys  
 145 150 155 160

Leu Ala Asn Glu Glu Leu Glu Val Arg Lys Glu Glu Ala Leu Ile Leu  
 165 170 175

Arg Thr Gln Ile Met Asn Ala Asp Gln Arg Arg Leu Ser Gly Lys Asn  
 180 185 190

Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys  
 195 200 205

His Val Asp Gln Glu Asp Ala Ile Glu Ala Tyr His Gly Val Cys Gln  
 210 215 220

Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln Ala Gln Ser Leu Glu His  
 225 230 235 240

Glu Glu Glu Val Glu His Leu Lys Ala Gln Val Glu Ala Leu Lys Glu  
 245 250 255

Glu Met Asp Lys Gln Gln Thr Phe Cys Gln Thr Leu Leu Leu Ser  
 260 265 270

Pro Glu Ala Gln Val Glu Phe Gly Val Gln Gln Glu Ile Ser Arg Leu  
 275 280 285

Thr Asn Glu Asn Leu Asp Phe Lys Glu Leu Val Glu Lys Leu Glu Lys  
 290 295 300

Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Val  
 305 310 315 320

Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala Gln Ser Asp Arg Arg His  
 325 330 335

His Glu Leu Thr Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe  
 340 345 350

Gln Gly Met Leu Glu Tyr His Lys Glu Val Glu Ala Leu Leu Ile Arg  
 355 360 365

Asn Leu Val Thr Asp Leu Lys Pro Gln Met Leu Leu Gly Thr Val Pro  
 370 375 380

Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr  
 385 390 395 400

Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn  
 405 410 415

Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr  
 420 425 430

Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln  
 435 440 445

Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn  
 450 455 460

Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu  
 465 470 475 480

Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu  
 485 490 495

Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser  
 500 505 510

Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser  
 515 520 525

Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp  
 530 535 540

Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe  
 545 550 555 560

Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Arg Lys Asp  
 565 570 575

Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln  
 580 585 590

Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val  
 595 600 605

Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys  
 610 615 620

Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser  
 625 630 635 640

Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu  
 645 650 655

Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln  
 660 665 670

Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser  
 675 680 685

Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr  
 690 695 700

Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn  
 705 710 715 720

Glu Val

<210> 123

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 BAR gene sequence

<220>

<221> CDS

<222> (1)...(549)

<400> 123

agc cca gaa cga cgc ccg gcc gac atc cgc cgt gcc acc gag gcg gac  
 Ser Pro Glu Arg Arg Pro Ala Asp Ile Arg Arg Ala Thr Glu Ala Asp  
 1 5 10 15

48

atg ccg gcg gtc tgc acc atc gtc aac cac tac atc gag aca agc acg  
 Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr  
 20 25 30

96

gtc aac ttc cgt acc gag ccg cag gaa ccg cag gag tgg acg gac gac  
 Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp  
 35 40 45

144

ctc gtc cgt ctg cgg gag cgc tat ccc tgg ctc gtc gcc gag gtg gac  
 Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp  
 50 55 60

192

ggc gag gtc gcc ggc atc gcc tac gcg ggc ccc tgg aag gca cgc aac  
 Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn  
 65 70 75 80

240

gcc tac gac tgg acg gcc gag tcg acc gtg tac gtc tcc ccc cgc cac  
 Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His  
 85 90 95

288

cag	cg	ac	gg	ct	gg	tcc	ac	ct	ta	ac	ca	ct	ct	aag	tcc	336
Gln	Arg	Thr	Gly	Leu	Gly	Ser	Thr	Leu	Tyr	Thr	His	Leu	Leu	Lys	Ser	
100								105					110			
ctg	gag	gca	cag	ggc	tcc	aag	agc	gtg	gtc	gct	gtc	atc	ggg	ctg	ccc	384
Leu	Glu	Ala	Gln	Gly	Phe	Lys	Ser	Val	Val	Ala	Val	Ile	Gly	Leu	Pro	
115								120				125				
aac	gac	ccg	agc	gtg	cgc	atg	cac	gag	gcg	ctc	gga	tat	gcc	ccc	cgc	432
Asn	Asp	Pro	Ser	Val	Arg	Met	His	Glu	Ala	Leu	Gly	Tyr	Ala	Pro	Arg	
130							135					140				
ggc	atg	ctg	cg	g	cc	ttc	aag	ca	gg	aa	tgg	cat	gac	gtg	480	
Gly	Met	Leu	Arg	Ala	Ala	Gly	Phe	Lys	His	Gly	Asn	Trp	His	Asp	Val	
145						150			155			160				
gg	tt	tc	tg	ca	ct	gac	tt	ac	ct	cc	gt	cc	cg	gt	528	
Gly	Phe	Trp	Gln	Leu	Asp	Phe	Ser	Leu	Pro	Val	Pro	Pro	Arg	Pro	Val	
165						170					175					
ctg	cc	gtc	ac	gaa	atc	tga									549	
Leu	Pro	Val	Thr	Glu	Ile											
180																

&lt;210&gt; 124

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
BAR gene sequence

&lt;400&gt; 124

Ser Pro Glu Arg Arg Pro Ala Asp Ile Arg Arg Ala Thr Glu Ala Asp  
1 5 10 15Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr  
20 25 30Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp  
35 40 45Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp  
50 55 60Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn  
65 70 75 80Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His  
85 90 95

Gln Arg Thr Gly Leu Gly Ser Thr Leu Tyr Thr His Leu Leu Lys Ser  
 100 105 110

Leu Glu Ala Gln Gly Phe Lys Ser Val Val Ala Val Ile Gly Leu Pro  
 115 120 125

Asn Asp Pro Ser Val Arg Met His Glu Ala Leu Gly Tyr Ala Pro Arg  
 130 135 140

Gly Met Leu Arg Ala Ala Gly Phe Lys His Gly Asn Trp His Asp Val  
 145 150 155 160

Gly Phe Trp Gln Leu Asp Phe Ser Leu Pro Val Pro Pro Arg Pro Val  
 165 170 175

Leu Pro Val Thr Glu Ile  
 180

<210> 125

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(363)

<400> 125

atg gga aaa ggt gtg aaa tcc ccg ggg gag aag tca cgc tat gag acc  
 Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr  
 1 5 10 15

48

tca ctg aat ctg acc acc aag cgc ttc ctg gag ctg ctg agc cac tcg  
 Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser  
 20 25 30

96

gct gac ggt gtc gtc gac ctg aac tgg gct gcc gag gtg ctg aag gtg  
 Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val  
 35 40 45

144

cag aag cgg cgc atc tat gac atc acc aac gtc ctt gag ggc atc cag  
 Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln  
 50 55 60

192

ctc att gcc aag aag tcc aag aac cac atc cag tgg ctg ggc agc cac  
 Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His  
 65 70 75 80

240

acc aca gtg ggc gtc ggc gga cgg ctt gag ggg ttg acc cag gac ctc  
 Thr Thr Val Gly Val Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu  
 85 90 95

288

cga cag ctg cag gag agc gag cag cag ctg gac cac ctg atg aat atc	336																																																																
Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile																																																																	
100	105	110		tgt act acg cag ctg cgc ctg ctc tcc tga	366	Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120	<210> 126		<211> 121		<212> PRT		<213> Homo sapiens		<400> 126		Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr		1	5	10	15	Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser		20	25	30		Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val		35	40	45		Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln		50	55	60		Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His		65	70	75	80	Thr Thr Val Gly Val Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu		85	90	95		Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile		100	105	110		Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120
110																																																																	
tgt act acg cag ctg cgc ctg ctc tcc tga	366																																																																
Cys Thr Thr Gln Leu Arg Leu Leu Ser																																																																	
115	120																																																																
<210> 126																																																																	
<211> 121																																																																	
<212> PRT																																																																	
<213> Homo sapiens																																																																	
<400> 126																																																																	
Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr																																																																	
1	5	10	15	Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser		20	25	30		Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val		35	40	45		Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln		50	55	60		Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His		65	70	75	80	Thr Thr Val Gly Val Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu		85	90	95		Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile		100	105	110		Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120																						
10	15																																																																
Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser																																																																	
20	25	30		Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val		35	40	45		Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln		50	55	60		Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His		65	70	75	80	Thr Thr Val Gly Val Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu		85	90	95		Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile		100	105	110		Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120																												
30																																																																	
Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val																																																																	
35	40	45		Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln		50	55	60		Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His		65	70	75	80	Thr Thr Val Gly Val Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu		85	90	95		Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile		100	105	110		Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120																																		
45																																																																	
Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln																																																																	
50	55	60		Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His		65	70	75	80	Thr Thr Val Gly Val Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu		85	90	95		Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile		100	105	110		Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120																																								
60																																																																	
Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His																																																																	
65	70	75	80	Thr Thr Val Gly Val Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu		85	90	95		Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile		100	105	110		Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120																																														
75	80																																																																
Thr Thr Val Gly Val Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu																																																																	
85	90	95		Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile		100	105	110		Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120																																																				
95																																																																	
Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile																																																																	
100	105	110		Cys Thr Thr Gln Leu Arg Leu Leu Ser		115	120																																																										
110																																																																	
Cys Thr Thr Gln Leu Arg Leu Leu Ser																																																																	
115	120																																																																